

QY 298 CGCTGTAGAGAAAGCTTCCAGTACATTGACCTCCATCAGAGATGAATTTTGACAGAGC 357
DB 327 CGCTGTAGAGAAAGCTTCCAGTACATTGACCTCCATCAGAGATGAATTTTGACAGAGC 386
QY 358 TGAAGAGTGGGTGGCCATCGAGAGCACTGTGCTCAGCTGTGCTTCAAGCAG 417
DB 387 TGAAGAGTGGGTGGCCATCGAGAGCACTGTGCTCAGCTGTGCTTCAAGCAG 446
QY 418 AGCTTTTCAAGATGATGCGCGCTGCGGACACGCTGAGAGCGCTGGGGGGCGCGGTGG 477
DB 447 AGCTTTTCAAGATGATGCGCGCTGCGGACACGCTGAGAGCGCTGGGGGGCGCGGTGG 506
QY 478 CCGTGGTGGACATGGGTCTCTGACAGCTCCGAGTGTGAGAGTCTTCAATACCTCCG 537
DB 507 CCGTGGTGGACATGGGTCTCTGACAGCTCCGAGTGTGAGAGTCTTCAATACCTCCG 566
QY 538 TCATCTGCGCCGAACTG 554
DB 567 TCATCTGCGCCGAACTG 583

RESULT 2

US-09-513-999C-13950
Sequence 13950 Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Sheelart, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13950
LENGTH: 300
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 67
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 68
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 69
OTHER INFORMATION: m=a or c
US-09-513-999C-13950

Query Match 8.0%; Score 180; DB 4; Length 300;
Best Local Similarity 99.6%; Pred. No. 4.5e-66;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 TTCCTTCGCGGGGCAACGTTGGGTCAAGGCAAGAGAGATTTAATGTCACCTCTTGG 125
DB 70 TTCCTTCGCGGGGCAACGTTGGGTCAAGGCAAGAGAGATTTAATGTCACCTCTTGG 129
QY 126 GGCCTTTCATGGGATCTCCTCTGCGCAATTTTGGAGTTGGGAAAGTTGTAAGGCTT 185
DB 130 GGCCTTTCATGGGATCTCCTCTGCGCAATTTTGGAGTTGGGAAAGTTGTAAGGCTT 189
QY 186 CAGAACTCCAGCTAATGATCCCAACTCGGAGAAATGGCTGCTCCTGCTGGCTGTG 245

DB 190 CAGAACTCCAGCTAATGATCCCAACTCGGAGAAATGGCTGCTCCTGCTGGCTGTG 249
QY 246 CTGCTGCTGCTGCTGAGCGGCGCATGTTCTCCTCACTCCCGCCCGCCG 296
DB 250 CTGCTGCTGCTGCTGAGCGGCGCATGTTCTCCTCACTCCCGCCCGCCG 300

RESULT 3

US-09-073-569-1
Sequence 1 Application US/09073569
Patent No. 6084088
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 34..1344
OTHER INFORMATION:

US-09-073-569-1

Query Match 2.7%; Score 61; DB 3; Length 1733;
Best Local Similarity 100.0%; Pred. No. 2.9e-16;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2182 CTCCTCCAAAAA
DB 1603 CTCCTCCAAAAA
QY 2242 A 2242
DB 1663 A 1663

RESULT 4
US-09-621-976-8550
Sequence 8550 Application US/09621976
Patent No. 6639063

~~us-10-036-342-56.rst~~

FEATURES

SOURCE

1.772

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/organism="Homo sapiens"
/mol_type="mRNA"
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/dd_xref="taxon:9606"  
/clone="IMAGE:5173289"  
/lab_host="DH10B"
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/clone_11b="NIH_MGC_115"  
/note="Organ: pooled brain"
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PCWV-SG006, site 1: Notti, site 2: EGNV, destroyed). RNA source anonymous pool of 6 male brains, age range 23-27, 1 male lung, age 27, and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (ECNV, site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Garber (Invitrogen). Research Genetics tracking code 321. Note: this is a NIH MGC Library."

ORIGIN

Query Match	25.7%	Score 577	DB 4	Length 772
Best Local Similarity	100.0%	Pred. No. 1e-270		
Matches 577	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	217	GGAGAAATGGCGCGCCTCCCTGGTGGCGTGAGCTGCTGCTGCTGGAGGGCGGCAAGTCT	276
Db	47	GGAGAAATGGCTGCGCTCCCTGCTGGCTGCTGCTGCTGCTGGAGGGCGGCAAGTCT	106
QY	277	CCTGACCCCTCCCGCCGCCCGCGCTGTATGAGAAAGCTTCCAGTACATTTGACCTCCATC	336
Db	107	CCTGACCCCTCCCGCCGCCCGCGCTGTATGAGAAAGCTTCCAGTACATTTGACCTCCATC	166
QY	337	AGGATGAATTTGTGACAGCGCTGAAGAGTGGGTGGCCATGAGAGCACTTGTCCAGC	396
Db	167	AGGATGAATTTGTGACAGCGCTGAAGAGTGGGTGGCCATGAGAGCACTTGTCCAGC	226
QY	397	CTGTGCGCTCGCTTGACAAAGAGCTCTCAAAATGATGGCCGTGGCTGCGGACACGCTGC	456
Db	227	CTGTGCGCTCGCTTGACAAAGAGCTCTCAAAATGATGGCCGTGGCTGCGGACACGCTGC	286
QY	457	AGCGCCTGGGGGGCCCGTGTGGCTTCGTGGGACATGGGTCTTCAGACAGCTGCCGATGTGC	516
Db	287	AGCGCCTGGGGGGCCCGTGTGGCTTCGTGGGACATGGGTCTTCAGACAGCTGCCGATGTGC	346
QY	517	AGATCTTCCAAATACCTTCCCGTCATCTGTGCGCGAACTGGGGAGCGATCTCCAGAAAGCA	576
Db	347	AGATCTTCCAAATACCTTCCCGTCATCTGTGCGCGAACTGGGGAGCGATCTCCAGAAAGCA	406
QY	577	CCGTGTGCTTTAAGGCGCACTTGGACGCGGACGCGTGCAGACCGGGGGCGATGGGTGGCTCA	636
Db	407	CCGTGTGCTTTAAGGCGCACTTGGACGCGGACGCGTGCAGACCGGGGGCGATGGGTGGCTCA	466

RESULT 11
AT939620/c

~~FOCUS~~

DEFINITION

ACCESSION
VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE

TITLE

JOURNAL
COMMENT

FEATURES

Source

ОБЪЕКТ

ORIGIN

Query Match 25.7%; Score 576; DB 1; Length 742;
 Best Local Similarity 100.0%; Pred. No. 3.1e-270;
 Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1288 CAGTATCCCTGGCCGAGTATAGAAAATTTTCATTCCTAGTCCCTCAGATG 1347
 609 CAGTATCCCTGGCCGAGTATAGAAAATTTTCATTCCTAGTCCCTCAGATG 550
 1348 TGTCTCGGTGAGAAAACAGTGACACGACATCTTGAGAGATGTTCTCCAAAAGAAATA 1407
 549 TGTCTCGGTGAGAAAACAGTGACACGACATCTTGAGAGATGTTCTCCAAAAGAAATA 490
 1408 GTTCCAAAGATGTTGTTTTCATGACTCTAGACACACCCGATGCAAAATATG 1467
 489 GTTCCAAAGATGTTGTTTTCATGACTCTAGACACACCCGATGCAAAATATG 430
 1468 ATGACACCCAGTATCTCGAGAGAAAAGGAGATCAGAACATGTTTGAACAGACAG 1527
 429 ATGACACCCAGTATCTCGAGAGAAAAGGAGATCAGAACATGTTTGAACAGACAG 370
 1528 ATATATCCGGAGATGATCACCATTCCAAATGTCAGAGAGATCGTCCACA 1587
 369 ATATATCCGGAGATGATCACCATTCCAAATGTTCCAGAGATCGTCCACA 310
 1588 AGAGCTGTGTCTAATTCCTGAGAGCTGTGATGATGAGAACATTCGAGATGAGA 1647
 309 AGAGCTGTGTCTAATTCCTGAGAGCTGTGATGATGAGAACATTCGAGATGAGA 250
 1648 AATATCAAGATGAGTATAGAGAGAGAACCAATTTATGCTGCTTTTCTTAGAGA 1707
 249 AATATCAAGATGAGTATAGAGAGAGAACCAATTTATGCTGCTTTTCTTAGAGA 190
 1708 TGGCCAGCTCATTATACAGAGACCTTCTAGTCTGATGATCAGATGCAAGATTC 1767
 189 TGGCCAGCTCATTATACAGAGACCTTCTAGTCTGATGATCAGATGCAAGATTC 130
 1768 CCTCCCAATCTCTTACAGAGAGATGATGATGATGATGATGATGATGATGATG 1827
 129 CCTCCCAATCTCTTACAGAGAGATGATGATGATGATGATGATGATGATGATG 70
 1828 TAGTACATTTTCCCTCATTAAATGCTTTGGA 1863
 69 TAGTACATTTTCCCTCATTAAATGCTTTGGA 34

RESULT 12
 BM669584/c
 LOCUS 630 bp mRNA linear EST 27-FEB-2002
 DEFINITION UI-E-DX1-agw-1-19-0-UI s1 UI-E-DX1 Homo sapiens cDNA clone
 UI-E-DX1-agw-1-19-0-UI 3', mRNA sequence.
 ACCESSION BM669584
 VERSION BM669584.1 GI:18979481
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 630)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL MEDLINE
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hegeman

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES

source

Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="fetal eyes"
 /dev_stage="fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_id="UI-E-DX1"
 /note="Organ: eye; Vector: pUT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-DX1 is a normalized cDNA library containing the
 following tissue(s): fetal eyes. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pUT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AGAATCAAGA. This library was created for the program Gene
 Discovery in the Visual System, supported by National Eye
 Institute (NEI).
 TAG_TISSUE=human fetal eyes
 TAG_LIB=UI-E-DX1
 TAG_SEQ=AGAATCAAGA"

ORIGIN

Query Match 25.4%; Score 570; DB 4; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2.7e-267;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1605 CCGCTGGAGCTGTGATGATGAGAAATTCGACAGATGAGAAATCAAGGTGAG 1664
 587 CCGCTGGAGCTGTGATGATGAGAAATTCGACAGATGAGAAATCAAGGTGAG 528
 1665 TACATAGAGGAAACCAATTAATTTGCTGCTTTTCTTAGAGATGAGCCAGCTCA 1724
 527 TACATAGAGGAAACCAATTAATTTGCTGCTTTTCTTAGAGATGAGCCAGCTCA 468
 1725 TCACAAAGAACCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1784
 467 TCACAAAGAACCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 408
 1785 GACAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1844
 407 GACAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
 1845 CATTAAATGCTTGGATATCTGGATCAGTAAATATTTTCAAGGCAAGATGTT 1904
 347 CATTAAATGCTTGGATATCTGGATCAGTAAATATTTTCAAGGCAAGATGTT 288
 1905 GGAATGCTTAAAGTCCCTCCAGCTGACACCTTCTCAAGTATGCTGTCAGCAAC 1964
 287 GGAATGCTTAAAGTCCCTCCAGCTGACACCTTCTCAAGTATGCTGTCAGCAAC 228
 1965 TTGATTTCCCAAGTCTGTGATAGCCCGAGATGATGATGATGATGATGATGAT 2024
 227 TTGATTTCCCAAGTCTGTGATAGCCCGAGATGATGATGATGATGATGATGAT 168
 2025 TATCTCAACCTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 2084
 167 TATCTCAACCTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 108